```
  1  GCACGAGGAACAGAACACTTTCTCATGTCCAGGGTCAGATTACAAGAGCACTCAAGACTT   60

 61  TACTGACGAAAACTCAGGAAATCCTCTATCACAAAGAGGTTTGGCAACTAAACTAAGACA  120

121  TTAAAAGGAAAATACCAGATGCCACTCTGCAGGCTGCAATAACTACTACTTACTGGATAC  180

181  ATTCAAACCCTCCAGAATCAACAGTTATCAGGTAACCAACAAGAAATGCAAGCCGTCGAC  240
  1                                                  M  Q  A  V  D    5

241  AATCTCACCTCTGCGCCTGGGAACACCAGTCTGTGCACCAGAGACTACAAAATCACCCAG  300
  6   N  L  T  S  A  P  G  N  T  S  L  C  T  R  D  Y  K  I  T  Q   25

301  GTCCTCTTCCCACTGCTCTACACTGTCCTGTTTTTTGTTGGACTTATCACAAATGGCCTG  360
 26   V  L  F  P  L  L  Y  T  V  L  F  F  V  G  L  I  T  N  G  L   45

361  GCGATGAGGATTTTCTTTCAAATCCGGAGTAAATCAAACTTTATTATTTTTCTTAAGAAC  420
 46   A  M  R  I  F  F  Q  I  R  S  K  S  N  F  I  I  F  L  K  N   65

421  ACAGTCATTTCTGATCTTCTCATGATTCTGACTTTTCCATTCAAAATTCTTAGTGATGCC  480
 66   T  V  I  S  D  L  L  M  I  L  T  F  P  F  K  I  L  S  D  A   85

481  AAACTGGGAACAGGACCACTGAGAACTTTTGTGTGTCAAGTTACCTCCGTCATATTTTAT  540
 86   K  L  G  T  G  P  L  R  T  F  V  C  Q  V  T  S  V  I  F  Y   105

541  TTCACAATGTATATCAGTATTTCATTCCTGGGACTGATAACTATCGATCGCTACCAGAAG  600
106   F  T  M  Y  I  S  I  S  F  L  G  L  I  T  I  D  R  Y  Q  K   125

601  AcCACCAGGCCATTTAAAACATCCAACCCCAAAAATCTCTTGGGGGCTAAGATTCTCTCT  660
126   T  T  R  P  F  K  T  S  N  P  K  N  L  L  G  A  K  I  L  S   145

661  GTTGTCATCTGGGCATTCATGTTCTTACTCTCTTtGCCTAACATGATTCTGACCAACAGg  720
146   V  V  I  W  A  F  M  F  L  L  S  L  P  N  M  I  L  T  N  R   165

721  CAGCCGAGAGACAAGAATGTGaAGAAaTGCTCTTTCCTTAAATCAGAGTTCGGTCTAGTC  780
166   Q  P  R  D  K  N  V  K  K  C  S  F  L  K  S  E  F  G  L  V   185

781  TGGCATGAAATAGTAAATTACATCTGTCAAGTCATTTTCTGGATTAATTTCTTAATTGTT  840
186   W  H  E  I  V  N  Y  I  C  Q  V  I  F  W  I  N  F  L  I  V   205
```

FIG.1A

```
841  ATTGTATGTTATACACTCATTACAAAAGAACTGTACCGGTCATACGTAAGAACGAGGGGT  900
206   I  V  C  Y  T  L  I  T  K  E  L  Y  R  S  Y  V  R  T  R  G   225

901  GTAGGTAAAGTCCCCAGGAAAAAGGTGAACGTCAAAGTTTTCATTATCATTGCTGTATTC  960
226   V  G  K  V  P  R  K  K  V  N  V  K  V  F  I  I  I  A  V  F   245

961  TTTATTTGTTTTGTTCCTTTCCATTTTGCCCGAATTCCTTACACCCTGAGCCAAACCCGG  1020
246   F  I  C  F  V  P  F  H  F  A  R  I  P  Y  T  L  S  Q  T  R   265

1021 GATGTCTTTGACTGCACtGcTGAAAATACTCTGTTCTATGTGAAAGAGAGCACTCTGTGG  1080
266   D  V  F  D  C  T  A  E  N  T  L  F  Y  V  K  E  S  T  L  W   285

1081 TTAACTTCCTTAAATGCATGCCTGGATCCGTTCATCTATTTTTTCCTTTGCAAGTCCTTC  1140
286   L  T  S  L  N  A  C  L  D  P  F  I  Y  F  F  L  C  K  S  F   305

1141 AGAAATTCCTTGATAAGTATGCTGAAGTGCCCCAATTCTGCAACATCTCTGTCCCAGGAC  1200
306   R  N  S  L  I  S  M  L  K  C  P  N  S  A  T  S  L  S  Q  D   325

1201 AATAGGAAAAAAGAACAGGATGGTGGTGAcCCAAATGAAGAGACTCCAATGTAAACAAAT  1260
326   N  R  K  K  E  Q  D  G  G  D  P  N  E  E  T  P  M  *         343

1261 TAACTAAGGAAATATTTCAATCTCTTTGTGTTCAGAACTCGTTAAAGCAAAGCGCTAAGT  1320

1321 AAAAATATTAACTGACGAAGAAGCAACTAAGTTAATAATAATGACTCTAAAGAAACAGAA  1380

1381 GATTACAAAAGCAATTTTCATTTACCTTTCCAGTATGAAAAGCTATCTTAAAATATAGAA  1440

1441 AACTAATCTAAACTGTAGCTGTATTAGCAGCAAAACAAACGACATCCAATTGTCATGCTG  1500

1501 CATGCAAAACTACACAGAATTCATGTTTTGgCAGAGTTTTGGCAAAATGAGTAATCATAT  1560

1561 AATATTTACTGTAATTTTTAAAATACATTATCGTTCACAATTTTATTTTTTTCATAATCAA  1620

1621 CTAAGGAAGAACGATCAATTGGATATAATCTTCTTACCAAAAATGATAGTTAAAATGTAT  1680

1681 ATATATCCTAGTCCCCTAACCaAATCCTGACCTATTGGGATACTTATAAAAATTTAAGTA  1740

1741 AGTGGGATACACAAAGAATAATAACTATTAACTTTTCATTATTAGCcAAAAACCTAAGGG  1800
```

FIG.1B

1801 ATTTAAACTAATTGAAaCTGTATTTGATTGGACTTAATTTTTTATGTTTATTTAGAAGAT 1860

1861 AAAGATTTAAGAAGACCTTTACAATAAAGAGAAGAAATATCGAAGTCATTAAAATAAGGA 1920

1921 GACTTACTTTTATGACATTCTAATACTAAAAAATATAGAAATATTTCCTTAATTCTAGAG 1980

1981 AAACTAGTTTTACTAATTTTTTACAACTTCAATAATACCATCACTGACACTTACCTTTAT 2040

2041 TAATTAGCTTCTAGAAAATAGCTGCTAATTAGGTTAATGAACATTTTACCTTAGTGAAAA 2100

2101 AAAaTTAATTAAATATGATTACAAAGTTGCACAGCATAACTACTGAGAGGAAAGTGATTG 2160

2161 ATCTGTTTGTAATTACTTGTTTGTATTGGTGTGTATAAAATACAAATTTACATTAAACTC 2220

2221 TAAAtcattaaaAAAAAAAAAAAAAAAA 2247

FIG.1C

```
  1 MQAVDNLTSAP....GNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLA  46
    :| .:|:|.:.    ||.:      .........:::|| |.::|::||:.| ||
  3 IQMANNFTPPSATPQGNDCDLYAHHSTARIVMPLHYSLVFIIGLVGNLLA  52


 47 MRIFFQIRSKSN.FIIFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTF  95
    : ::.| |.| |   .:: .| ||||:|:. .:| :|   |. . .: .
 53 LVVIVQNRKKINSTTLYSTNLVISDILFTTALPTRIAYYAMGFDWRIGDA  102


 96 VCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKILS  145
    :|.:|.::||:.  |  :::.|:.  :.|||:   ..:::  ..  |.:  || ::
103 LCRITALVFYINTYAGVNFMTCLSIDRFIAVVHPLRYNKIKRIEHAKGVC  152


146 VVIWAFMFLLSLPNMI..LTNRQPRDKNVKKCSFLKSEFGLVWHEIVNYI  193
    :..:| ::|  .|| :|   :...::     ....:. :... :|.|   :...::
153 IFVWILVFAQTLPLLINPMSKQEAERITCMEYPNFEETKSLPWILLGACF  202


194 CQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGK..VPRKKVNVKVFII  241
    .. :: :::|:::||. |. .|:|. ... .:| | :| :|. ::||
203 IGYVL..PLIIILICYSQICCKLFRTAKQNPLTEKSGVNKKALNTIILII  250


242 IAVFFICFVPFHFARIPYTLSQTR..DVFDCTAENTLFYVKESTLWLTSL  289
    : ||.:||.|:|.| |.. :.. |  :.::|.. :.: .  . |: | .:
251 V.VFVLCFTPYHVAIIQHMIKKLRFSNFLECSQRHSFQISLHFTVCLMNF  299


290 NACLDPFIYFFLCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEE  339
    |.|:|||||||| ||:::..::.||| . | .|:| . :. .::.: . .|
300 NCCMDPFIYFFACKGYKRKVMRMLKRQVS.VSISSAVKSAPEENSREMTE  348


340 TPM 342
    |.|
349 TQM 351
```

FIG.2

```
  1  GGCACGAGCCCACCCTGCGTCGGGCCTCAGTCAGCCCCCGGGGGAGGCCATGAACGCCAC   60
  1                                                   M   N   A   T    4

 61  GGGGACCCCGGTGGCCCCCGAGTCCTGCCAACAGCTGGCGGCCGGCGGGCACAGCCGGCT  120
  5   G   T   P   V   A   P   E   S   C   Q   Q   L   A   A   G   G   H   S   R   L   24

121  CATTGTTCTGCACTACAACCACTCGGGCCGGCTGGCCGGGCGCGGGGGGCCGGAGGATGG  180
 25   I   V   L   H   Y   N   H   S   G   R   L   A   G   R   G   G   P   E   D   G   44

181  CGGCCTGGGGGCCCTGCGGGGGCTGTCGGTGGCCGCCAGCTGCCTGGTGGTGCTGGAGAA  240
 45   G   L   G   A   L   R   G   L   S   V   A   A   S   C   L   V   V   L   E   N   64

241  CTTGCTGGTGCTGGCGGCCATCACCAGCCACATGCGGTCGCAACGCTGGGTCTACTATTG  300
 65   L   L   V   L   A   A   I   T   S   H   M   R   S   Q   R   W   V   Y   Y   C   84

301  CCTGGTGAACATTACGATGAGTGACCTGCTCACGGGCGCGGCCTACCTGGCCAACGTGCT  360
 85   L   V   N   I   T   M   S   D   L   L   T   G   A   A   Y   L   A   N   V   L   104

361  GCTGTCGGGGGCCCGCACCTTCCGTCTGGCGCCCGCCCAGTGGTTCCTACGGAAGGGCCT  420
105   L   S   G   A   R   T   F   R   L   A   P   A   Q   W   F   L   R   K   G   L   124

421  GCTCTTCACCGCCCTGGCCGCCTCCACCTTCAGCCTGCTCTTCACTGCAGGGTTGCGCTT  480
125   L   F   T   A   L   A   A   S   T   F   S   L   L   F   T   A   G   L   R   F   144

481  TGCCACCATGGTGCGGCCGGTGGCCGAGAGCGGGGCCACCAAGACCAGCCGCGTCTACGG  540
145   A   T   M   V   R   P   V   A   E   S   G   A   T   K   T   S   R   V   Y   G   164

541  CTTCATCGGCCTCTGCTGGCTGCTGGCCGCGCTGCTGGGGATGCTGCCTTTGCTGGGCTG  600
165   F   I   G   L   C   W   L   L   A   A   L   L   G   M   L   P   L   L   G   W   184

601  GAACTGCCTGTGCGCCTTTGACCGCTGCTCCAGCCTTCTGCCCCTCTACTCCAAGCGCTA  660
185   N   C   L   C   A   F   D   R   C   S   S   L   L   P   L   Y   S   K   R   Y   204

661  CATCCTCTTCTGCCTGGTGATCTTCGCCGGCGTCCTGGCCACCATCATGGGCCTCTATGG  720
205   I   L   F   C   L   V   I   F   A   G   V   L   A   T   I   M   G   L   Y   G   224

721  GGCCATCTTCCGCCTGGTGCAGGCCAGCGGGCAGAAGGCCCCCACGCCCAGCGGCCCGCCG  780
225   A   I   F   R   L   V   Q   A   S   G   Q   K   A   P   R   P   A   A   R   R   244
```

FIG.3A

781 CAAGGCCCGCCGCCTGCTGAAGACGGTGCTGATGATCCTGCTGGCCTTCTTGGTGTGCTG 840
245 K   A   R   R   L   L   K   T   V   L   M   I   L   L   A   F   L   V   C   W 264

841 GGGACCACTCTTCGGGCTGCTGCTGGCCGACGTCTTTGGCTCCAACCTCTGGGCCCAGGA 900
265 G   P   L   F   G   L   L   L   A   D   V   F   G   S   N   L   W   A   Q   E 284

901 GTACCTGCGGGGCATGGACTGGATCCTGGCCCTGGCCGTCCTCAACTCGGCGGTCAACCC 960
285 Y   L   R   G   M   D   W   I   L   A   L   A   V   L   N   S   A   V   N   P 304

961 CATCATCTACTCCTTCCGCAGCAGGGAGGTGTGCAGAGCCGTGCTCAGCTTCCTCTGCTG 1020
305 I   I   Y   S   F   R   S   R   E   V   C   R   A   V   L   S   F   L   C   C 324

1021 CGGGTGTCTCCGGCTGGGCATGCGAGGGCCCGGGGACTGCCTGGCCCGGGCCGTCGAGGC 1080
325 G   C   L   R   L   G   M   R   G   P   G   D   C   L   A   R   A   V   E   A 344

1081 TCACTCCGGAGCTTCCACCACCGACAGCTCTCTGAGGCCAAGGGACAGCTTTCGCGGCTC 1140
345 H   S   G   A   S   T   T   D   S   S   L   R   P   R   D   S   F   R   G   S 364

1141 CCGCTCGCTCAGCTTTCGGATGCGGGAGCCCCTGTCCAGCATCTCCAGCGTGCGGAGCAT 1200
365 R   S   L   S   F   R   M   R   E   P   L   S   S   I   S   S   V   R   S   I 384

1201 CTGAAGTTGCAGTCTTGCGTGTGGATGGTGCAACCACCGGGTGCGTGCCAGGCAGGCCCT 1260
385 *   385

1261 CCTGGGGGTACAGGAAGCTGTGTGCACGCAACCTCGCCCTGTATGGGGAGCAGGGAACGGG 1320

1321 ACAGGCCCCCATGGACTTGCCCGGTGGCCTCTCGGGGCTTCTGACGCCATATGGACTTGC 1380

1381 CCATTGCCTATGGCTCACCCTGGACAAGGAGGCAACCACCCCACCTCCCCGTAGGAGCAG 1440

1441 AGAGCACCCTGGTGTGGGGGGCGAGTGGGTTCCCCACAACCCCGCTTCTGTGTGATTCTGG 1500

1501 GGAAGTCCCGGCCCCTCTCTGGGCCTCAGTAGGGCTCCCAGGCTGCAAGGGGTGGACTGT 1560

1561 GGGATGCATGCCCTGGCAACATTGAAGTTCGATCATGGTAAAAAAAAAAAAAAAAAAAAAA 1620

1621 AAAAAAAAAAAAAAAAA 1637

FIG.3B

```
  1  MNATGTPVAPESCQQLAAGGHSRLIVLHYNHSGRLAGRGGPEDGGLGALR   50
     |.:|:.|:...      :.. .:  :|| |||..|:|. .::.|:  ::     .
  1  MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISADKEN.SIKLTS   49


 51  GLSVAASCLVVLENLLVLAAITSHMRSQRWVYYCLVNITMSDLLTGAAYL  100
     .: :   :|:::|||::||  .|  . .:  :|  :|| :.|:.:||||.|.||
 50  VVFILICCFIILENIFVLLTIWKTKKFHRPMYYFIGNLALSDLLAGVAYT   99


101  ANVLLSGARTFRLAPAQWFLRKGLLFTALAASTFSLLFTAGLRFATMVRP  150
     ||:||||| |::|.||||||||.| :|.||.||.|||| .|  |: ||::
100  ANLLLSGATTYKLTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLKM  149


151  VAESGATKTSRVYGFIGLCWLLAALLGMLPLLGWNCLCAFDRCSSLLPLY  200
     ..|. .. |:: :|: ||::. :|| ||::||||::|:...||.:||||
150  KLHNGS.NNFRLFLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLY  198


201  SKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGQKAPRPAARRKARR..  248
      |:|||||  .:|. :|  .|:  ||. |:.||...:.:  .  .  .||.|
199  HKHYILFCTTVFTLLLLSIVILYCRIYSLVRTRSRRLTFRKNISKASRSS  248


249  ....LLKTVLMILLAFLVCWGPLFGLLLADVFGSNLWAQEYLRGMDWILA  294
         |||||:::| .|:.||:|||  |||  || |:.:..  :.|    :::|.
249  ENVALLKTVIIVLSVFIACWAPLFILLLLDV.GCKVKTCDILFRAEYFLV  297


295  LAVLNSAVNPIIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAVEA  344
     ||||||:.|||||.: .:|: ||.:.:::|.  .  |  :.:: : |:: |
298  LAVLNSGTNPIIYTLTNKEMRRAFIRIMSCCKCPSG..DSAGKFKRPIIA  345


345  ...HSGASTTDSSLRPRDSFRGSRSLSFRMREPLSSIS  379
        |  ....:||  ..:|.  |... .:. .: :.| |
346  GMEFSRSKSDNSSHPQKDE..GDNPETIMSSGNVNSSS  381
```

FIG.4